

TITLE: GENOTYPIC CHARACTERIZATION OF ANTIMICROBIAL RESISTANCE AND VIRULENCE FACTORS OF *SALMONELLA* HEIDELBERG ISOLATED FROM POULTRY IN BRAZIL

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ABSTRACT

S. Heidelberg is one of the most widely distributed serotypes worldwide and it is among the ten *Salmonella* serotypes most frequently associated with human diseases. The presence of this microbiological hazard affects negatively the poultry industry whereas Brazilian products of avian origin are exported to five continents. The overuses of antimicrobial agents in food animal production have contributed to the development of antimicrobial resistant pathogens such as *S. Heidelberg* that has emerged as a major public health implication. Furthermore, the presence of virulence genes plays an important role in bacterial pathogenicity. These genes confer advantages such as adaptation to the host cell, resistance to antimicrobials and the ability to overcome host defense mechanisms, making it difficult to control and treat salmonellosis. In total, sixteen poultry isolates identified as *S. Heidelberg* ST15 were included in this study belonging to 2012-2018 period. DNA was extracted using the Wizard Genomic DNA Purification kit. Whole-genome shotgun sequencing was performed using an Ion Torrent S5. Read trimming and assembly were performed using CLC Genomics Workbench v.11.0.1 software. For genotypic analysis, online tools of the Center for Genomic Epidemiology were used to determine in silico serotype, MLST and resistance genes. The major virulence factors and islands of pathogenicity of *Salmonella* were analyzed using Virulence Factor Database (VFDB) and SPIfinder, respectively. All strains showed resistance genes to ceftiofur (*bla_{CMY-2}*), aminoglycoside (*aac(6')-Iaa*), tetracycline (*tet(A)*), sulphonamide (*sul2*) and fosfomicin (*fosA7*). Four strains (25%) were positive to quinolones (*qnrB19*). In relation to virulence, all isolates were positive for *invA*, *csgA* and *lpfA*, *mgtB* and *mgtC*, *fimH*, *phoP* and *phoQ*, and *sipB*. These genes are involved in the processes of invasion of epithelial cells, bacterial adhesion, Mg²⁺ transport, host cell specific recognition, regulation and induction of apoptosis in macrophages by caspase-1 activation, respectively. SPI analysis revealed that all isolates harbored SPI1, SPI2, SPI3, SPI5 and SPI9. Also present in several isolates were SPI4, CS54 island and centisome 63 pathogenicity island (C63PI). Our study reinforces the importance of intensifying the monitoring of antimicrobial resistance and virulence factors in strains of *S. Heidelberg* circulating in poultry from Brazil, since this is the world's largest chicken exporting country.

Keywords: *Salmonella*; antimicrobial resistance; virulence factors; poultry.

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